

47-Activation of viral integrations following chromosome redistribution during an interspecific cross

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Most of present day edible bananas (*Musa* sp.) are the result of inter-specific hybridizations of two wild species *Musa acuminata* (A genome) and *Musa balbisiana* (B genome). *M. balbisiana* presents interesting agronomical characteristics such as resistance to biotic and abiotic stresses that are targeted during banana breeding programs. However, since the mid-90s, many *Banana streak virus* (BSV) outbreaks have occurred in banana-producing areas resulting from the activation of infectious BSV integrations (eBSVs) in newly created interspecific banana hybrids. Recently, we established that these problematic infectious eBSVs are present in the *M. balbisiana* genomes only. Over the last 10 years, we characterized the sequence and organization of eBSVs of four BSV species present in the seedy *Pisang Klutuk Wulung* (PKW) *M. balbisiana* diploid (Gayral et al., 2008 ; Chabannes et al., 2012). We showed for instance that eBSV Goldfinger (eBSGFV) and eBSV Obino l'ewai (eBSOLV) are di-allelic at one locus, with infectious and non-infectious alleles for each species. They are both present on chromosome 1 of PKW and up to now there is a lack of knowledge on genetic regulation of such infectious eBSV.

We monitored the distribution of infectious eBSV sequences among a F1 triploid AAB population produced by inter-specific cross between the tetraploid CRBP39 (AAAB) female parent and the male diploid *M. acuminata* (AA) Pahang. CRBP39 is a plantain carrying both infectious alleles of eBSGFV and eBSOLV while Pahang do not possess any eBSV for BSOLV and BSGFV. Results showed a strong bias in favor of hybrids containing chromosome 1 of *M. balbisiana* and demonstrated that interspecific chromosome recombination occur between *M. balbisiana* and *M. acuminata* genomes at least for chromosome 1. We are currently analyzing the distribution of chromosomes A and B in the resulting hybrids using microsatellites markers. This characterization is in progress and should allow getting an overview of the genetic structure of each offspring. This will help determined if the presence of particular chromosome segments could influence eBSV activation and thus whether the recombination and/or redistribution events of *M. Balbisiana* chromosomes in these hybrids could impact the recovery of a functional viral genome from eBSV. This should at term allow the safety re-introduction of B genome in banana breeding programs based on a reliable and early selection of risky hybrids.

Keywords: Breeding, plantain, BSV, eBSV, chromosome distribution, microsatellites, selection.

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